REMARKS

The Office Action of May 30, 2006 has been received and reviewed. Claims 1-18 are pending. Claims 10-17 were withdrawn from consideration. Claims 1-9 and 18 stand rejected. Claims 1, 2, 4-7, 9 and 18 have been amended as previously set forth. Claims 3 and 8 are to be canceled. All amendments and cancellations are made without prejudice or disclaimer. Reconsideration is respectfully requested.

Basis for amendment

Claim 1 has been amended to incorporate certain elements from claims 3 and 8. Basis for the amendment can be found throughout the specification, for example, in original claims 3 and 8.

Claims 4-7 have been amended to simply remove the element "of the NF-κB related pathway".

Claims 4, 7, 9 and 18 have been amended to directly depend from claim 1 since certain elements of claims 3 and 8 have been incorporated into claim 1.

No new matter has been introduced.

Objection to Specification

The specification has been amended to include updated priority data. Withdrawal of the objection is requested.

Objection to claims

Claims 3 and 8 have been canceled rendering the rejections as to them moot. The full spelling of "TNF" has been provided in claim 9 thus overcoming the objection.

Claim rejections – 35 USC § 112

Claims 1-9 and 18 were rejected under 35 USC § 112, second paragraph, as allegedly being indefinite. Claim 1 has been amended to replace "A-20 interacting proteins" with ABIN dependent NF-KB inhibition. An A20-interacting protein, specifically, a protein comprising the

amino acid sequence of SEQ ID NO:9, has been included in claim 1. The wording "interact" in claim 1 has been specified as "activate or suppress". In claims 1-2, 4-6 and 18, the wording "of an NF-κB related pathway" has been deleted. Claims 3 and 8 have been canceled rendering the rejection moot. In view of the amendments, applicants believe that claims 1-2, 4-7, 9 and 18 are clear and definite.

Claim rejections – 35 USC § 112

Claims 1, 2 and 18 were rejected under 35 USC § 112, first paragraph, as allegedly failing to comply with the written description requirement. Claim 1 has been amended to remove the wording "A20 interacting proteins". In claims 1, 2 and 18, the wording "of an NF-κB related pathway" has also been deleted. An A20-interacting protein, specifically in claim 1, a protein comprising the amino acid sequence of SEQ ID NO:9, has been included in that claim. In view of the amendments, applicants believe that the written description requirement is fully complied with, and withdrawal of the rejections is thus respectfully requested.

Scope of enablement rejection

Claims 1 and 2 were rejected under 35 USC § 112, first paragraph, for allegedly not meeting the enablement requirement. Claim 1 has been amended to include the admittedly enabled subject matter (a method that uses ABIN and ABIN2 (SEQ ID NO:9)). Claim 2 depends from claim 1 and further specifies that the protein of claim 1 comprises an A20 protein. Applicants believe that amended claims 1 and 2 are fully enabled. Withdrawal of the rejections is thus respectfully requested.

Claim rejections – 35 USC § 102

Claims 1 and 2 were rejected under 35 USC § 102(b) as allegedly being anticipated by Song et al. Claim 1 has been amended to specify the A-20 interacting protein as a protein comprising the amino acid sequence of SEQ ID NO:9. TRAF1/TRAF2 that interacts with A20 does not comprise SEQ ID NO:9. Therefore, the teachings from Song et al. should not anticipate claim 1. Withdrawal of the rejection is thus respectfully requested.

Each of claims 2 and 18 is not anticipated by Song et al. for, *inter alia*, depending from

claim 1.

Claim rejections – 35 USC § 103

Claims 3, 4, 6 and 7 were rejected under 35 USC § 103(a) as allegedly being unpatentable over Song et al. Applicants traverse the rejections as set forth hereinafter.

The Office Action argues that since TRAF2 binds to A20, and thus inherently must comprise SEQ ID NO:9, which is a consensus sequence. A search at the National Center for Biotechnology Information has revealed however that a *Homo sapiens* TNF receptor-associated factor 2 (TRAF2, gi:55959978) neither comprises SEQ ID NO:9, nor has a fragment that is an apparent consensus sequence of SEQ ID NO:9. Specifically, the sequence of TRAF2 and the conserved amino acid sequences of SEQ ID NO:9 have been aligned using Bioedit Sequence Alignment Editor. A pairwise alignment and an alignment report are enclosed herewith. It is to be noted that TRAF2 and SEQ ID NO:9 have an alignment score of -412. A report for the search results from NCBI is also enclosed herewith.

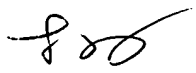
In addition, proteins that bind to A20 may bind to different parts of A20, and the binding interactions may be dictated by different mechanisms. As such, not all proteins that bind to A20 necessarily contain the same consensus sequence. Therefore, Song et al. does not, either explicitly or inherently, teach or suggest all claim elements of any one of claims 3, 4, 6 and 7.

The Office Action further argues that one of ordinary skill in the art would have been motivated to design SEQ ID NO:9 by a site mutagenesis method, since inherently it would have been obvious to deduce SEQ ID NO:9 from known sequences of TRAF2 that bind to A20. As discussed *supra*, TRAF2 does not inherently contain a consensus sequence of SEQ ID NO:9. It would be difficult to discover the part of the sequence of TRAF2 that interacts with A20. Since TRAF2 does not contain a fragment that is an apparent consensus sequence of SEQ ID NO:9, it would not be without undue experimentation to produce a consensus sequence of SEQ ID NO:9 by site mutagenesis even though the binding domain of TRAF2 is identified. Therefore, no reasonable expectation of success exists in modifying TRAF2 to produce SEQ ID NO: 9 by site mutagenesis.

In view of the foregoing, a *prima facie* case of obviousness has not been established for any of claims 3, 4, 6 and 7. Withdrawal of the rejections is thus respectfully requested.

If questions should remain after consideration of the foregoing, the Examiner is kindly requested to contact applicants' agent at the address or telephone number given herein.

Respectfully submitted,



Li Feng, Ph.D.
Registration No. 57,292
Agent for Applicant(s)
TRASKBRITT
P.O. Box 2550
Salt Lake City, Utah 84110-2550
Telephone: 801-532-1922

Date: July 25, 2006

Enclosure: Alignment
Pairwise alignment report
Search results for TNF receptor-associated factor 2

Document in ProLaw

Alignment: C:\BioEdit\Temp\~out.tmp

```
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                         10         20         30         40         50
TRAF2           ----maaasv tppgslellq pgfsktllgt kleakylcsa crnvlrrpfq
SEQ NO:9        lqqd------ ---------- ---------- ---------- ----------


                ....|....| ....|....| ....|....| ....|....| ....|....|
                        60         70         80         90        100
TRAF2           aqcghrycsf clasilssgp qncaacvheg iyeegisile sssafpdnaa
SEQ NO:9        ---------f ---------- ---------- ---------e ----------


                ....|....| ....|....| ....|....| ....|....| ....|....|
                       110        120        130        140        150
TRAF2           rreveslpav cpsdgctwkg tlkeyesche grcplmltec packglvrlg
SEQ NO:9        -r-------- ---d------ ---------- ---------- ----------


                ....|....| ....|....| ....|....| ....|....| ....|..
                       160        170        180        190
TRAF2           ekerhlehec perslscrhc rapccgadvk ahhevcpkfp ltcdgcg
SEQ NO:9        ---r------ -e-------- r--------- ---------- -------
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Pairwise Alignment
Sequence 1: TRAF2
Sequence 2: SEQ NO:9
Optimal Global aligment
Alignment score: -412

Identities: 0.0355330
Similarities: 0.0355330
Similarity Matrix: IDENTIFY

☐ 1: CAI15104. Reports TNF receptor-asso...[gi:55959978]

Comment Features Sequence

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VERSION     CAI15104.1  GI:55959978
DBSOURCE    embl accession AL355987.31
            embl accession AL449425.15
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (residues 1 to 193)
  AUTHORS   Brown,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr9
            RP11-523A20 is from the library RPCI-11.2 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            --------------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
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            one subclone; and the assembly was confirmed by restriction digest,
            except on the rare occasion of the clone being a YAC.
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                     /clone_lib="RPCI-11.2"
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                     /db_xref="CDD:34991"
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                     /locus_tag="RP11-523A20.1-002"
                     /standard_name="OTTHUMP00000022624"
                     /coded_by="join(AL355987.31:177226..177413,
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       61 ilssgpqnca acvhegiyee gisilesssa fpdnaarrev eslpavcpsd gctwkgtlke
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      181 vcpkfpltcd gcg
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